



IFWO

RAW SEQUENCE LISTING

DATE: 08/10/2004

PATENT APPLICATION: US/10/761,435A

TIME: 11:13:01

Input Set : A:\sequence.listing.txt

Output Set: N:\CRF4\08102004\J761435A.raw

3 <110> APPLICANT: Umana, Pablo
 4 Bruenker, Peter
 5 Ferrara, Claudia
 6 Suter, Tobias
 8 <120> TITLE OF INVENTION: Fusion Constructs and Use of Same to Produce Antibodies with
 9 Increased Fc Receptor Binding Affinity and Effector Function
 11 <130> FILE REFERENCE: 1975.0180003
 13 <140> CURRENT APPLICATION NUMBER: US 10/761,435A
 C--> 14 <141> CURRENT FILING DATE: 2004-01-22
 16 <150> PRIOR APPLICATION NUMBER: US 60/441,307
 17 <151> PRIOR FILING DATE: 2003-01-22
 19 <150> PRIOR APPLICATION NUMBER: US 60/491,254
 20 <151> PRIOR FILING DATE: 2003-07-31
 22 <150> PRIOR APPLICATION NUMBER: US 60/495,142
 23 <151> PRIOR FILING DATE: 2003-08-15
 25 <160> NUMBER OF SEQ ID NOS: 20
 27 <170> SOFTWARE: PatentIn version 3.2
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 30 <211> LENGTH: 11
 31 <212> TYPE: PRT
 32 <213> ORGANISM: Unknown
 34 <220> FEATURE:
 35 <223> OTHER INFORMATION: c-myc epitope tag
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 40 1 5 10
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 45 <212> TYPE: DNA
 46 <213> ORGANISM: Artificial Sequence
 48 <220> FEATURE:
 49 <223> OTHER INFORMATION: GAB-177 PCR primer
 51 <400> SEQUENCE: 2
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 55 <210> SEQ ID NO: 3
 56 <211> LENGTH: 26
 57 <212> TYPE: DNA
 58 <213> ORGANISM: Artificial Sequence
 60 <220> FEATURE:
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 63 <400> SEQUENCE: 3
 64 gaaggtttct ccagcaccct ggtacc 26
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82 <213> ORGANISM: Artificial Sequence
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85 <223> OTHER INFORMATION: GAB-180 PCR primer
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94 <213> ORGANISM: Artificial Sequence
96 <220> FEATURE:
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122 <220> FEATURE:
123 <223> OTHER INFORMATION: GAB-254 PCR primer
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128 gtcccc 66
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133 <212> TYPE: DNA
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155 <210> SEQ ID NO: 11
156 <211> LENGTH: 48
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158 <213> ORGANISM: Artificial Sequence
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168 <211> LENGTH: 1715
169 <212> TYPE: DNA
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172 <220> FEATURE:
173 <223> OTHER INFORMATION: Nucleotide sequence of GnTI-GnTIII
175 <400> SEQUENCE: 12
176 atgaagttaa gccgccagtt caccgtgttc ggcagtgcga tcttctgtgt ggtgattttc 60
178 tcgctctacc tgatgctgga ccgggggtcac ttagactacc ccaggaaccc gcgccgcgag 120
180 ggctccttcc ctcagggcca gctctcaatg ttgcaagaaa aaatagacca tttggagcgt 180
182 ttgctagctg agaataatga gatcatctca aatattagag actcagtcac caatttgagt 240
184 gagtctgtgg aggatgggtc gaaaagttca caaagcaatt tcagccaagg tgcgtgctca 300
186 cccctgctcc agccactgtc ccctagcaag gccacgcgaag aactgcaccg ggtggacttc 360
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190 aaaccaggta ccaggatgct ggagaaacct tctccagggc ggacagagga gaagaccaag 480
192 gtggctgagg ggtcctcggg ccgggggtcct gctcggaggc ctatgcggca tgtgttgagt 540
194 gcacgggagc gcctgggagg ccgggggcaact aggcgcgaagt ggggttgagt tgtgtgctg 600
196 ccaggctggc acggggccag ctgcgggggtg cccactgtgg tccagtattc caacctgcc 660
198 accaaggagc gcctggtacc caggggaggtg ccgaggcggg ttatcaacgc catcaacatc 720
200 aaccatgagt tcgacctgct ggatgtgcgc ttccatgagc tgggcgatgt tgtggacgcc 780
202 tttgtggtct gcgaatccaa ttccaccgcc tacggggagc ctcgccgct caagtccga 840
204 gagatgctga ccaatggcac cttcgagtac atccgccaca aggtgctcta cgtcttctg 900
206 gaccacttcc cacctggtgg ccgtcaggac ggetggattg cagacgacta cctgcgtacc 960
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212 ggctggacag agcccttcgc ctcccatatg cgcaagtccc tgtatggtt cttttggaag 1140
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216 ggctggacgg catccgctg cgccgcgctc agtactacac catgcccac tttcgacagt 1260
218 atgagaaccg caccgcccac atcctagtg agtggctctc cggcagcccc ctgcacttcg 1320
220 cgggctggca ctgctcctgg tgcctcacac ccgagggcac ctacttcaaa ctctgtcgg 1380
222 ccagaatgg tgacttcccc cgctgggggtg actacgagga caagagggac ctcaattaca 1440
224 tccgaagctt gattcgcact gggggatggt tcgacggcac gcagcaggag taccctcctg 1500
226 cagacccag tgaacacatg tatgctccta agtacctgct caagaactat gaccagttcc 1560

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228 gctacttgct cgaaaatccc taccgggagc ccaagagcac tgtagagggt gggcgccgga 1620
230 accagggctc agacggaagg tcattctgctg tcaggggcaa gttggatata acggagggcc 1680
232 cggaacagaa actgatctct gaagaggacc tgtag 1715
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236 <211> LENGTH: 571
237 <212> TYPE: PRT
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Amino acid sequence of GnTI-GnTIII
243 <400> SEQUENCE: 13
245 Met Lys Leu Ser Arg Gln Phe Thr Val Phe Gly Ser Ala Ile Phe Cys
246 1 5 10 15
249 Val Val Ile Phe Ser Leu Tyr Leu Met Leu Asp Arg Gly His Leu Asp
250 20 25 30
253 Tyr Pro Arg Asn Pro Arg Arg Glu Gly Ser Phe Pro Gln Gly Gln Leu
254 35 40 45
257 Ser Met Leu Gln Glu Lys Ile Asp His Leu Glu Arg Leu Leu Ala Glu
258 50 55 60
261 Asn Asn Glu Ile Ile Ser Asn Ile Arg Asp Ser Val Ile Asn Leu Ser
262 65 70 75 80
265 Glu Ser Val Glu Asp Gly Pro Lys Ser Ser Gln Ser Asn Phe Ser Gln
266 85 90 95
269 Gly Ala Gly Ser Pro Leu Leu Gln Pro Leu Ser Pro Ser Lys Ala Thr
270 100 105 110
273 Glu Glu Leu His Arg Val Asp Phe Val Leu Pro Glu Asp Thr Thr Glu
274 115 120 125
277 Tyr Phe Val Arg Thr Lys Ala Gly Gly Val Cys Phe Lys Pro Gly Thr
278 130 135 140
281 Arg Met Leu Glu Lys Pro Ser Pro Gly Arg Thr Glu Glu Lys Thr Lys
282 145 150 155 160
285 Val Ala Glu Gly Ser Ser Val Arg Gly Pro Ala Arg Arg Pro Met Arg
286 165 170 175
289 His Val Leu Ser Ala Arg Glu Arg Leu Gly Gly Arg Gly Thr Arg Arg
290 180 185 190
293 Lys Trp Val Glu Cys Val Cys Leu Pro Gly Trp His Gly Pro Ser Cys
294 195 200 205
297 Gly Val Pro Thr Val Val Gln Tyr Ser Asn Leu Pro Thr Lys Glu Arg
298 210 215 220
301 Leu Val Pro Arg Glu Val Pro Arg Arg Val Ile Asn Ala Ile Asn Ile
302 225 230 235 240
305 Asn His Glu Phe Asp Leu Leu Asp Val Arg Phe His Glu Leu Gly Asp
306 245 250 255
309 Val Val Asp Ala Phe Val Val Cys Glu Ser Asn Phe Thr Ala Tyr Gly
310 260 265 270
313 Glu Pro Arg Pro Leu Lys Phe Arg Glu Met Leu Thr Asn Gly Thr Phe
314 275 280 285
317 Glu Tyr Ile Arg His Lys Val Leu Tyr Val Phe Leu Asp His Phe Pro
318 290 295 300
321 Pro Gly Gly Arg Gln Asp Gly Trp Ile Ala Asp Asp Tyr Leu Arg Thr

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322 305          310          315          320
325 Phe Leu Thr Gln Asp Gly Val Ser Arg Leu Arg Asn Leu Arg Pro Asp
326          325          330          335
329 Asp Val Phe Ile Ile Asp Asp Ala Asp Glu Ile Pro Ala Arg Asp Gly
330          340          345          350
333 Val Leu Phe Leu Lys Leu Tyr Asp Gly Trp Thr Glu Pro Phe Ala Phe
334          355          360          365
337 His Met Arg Lys Ser Leu Tyr Gly Phe Phe Trp Lys Gln Pro Gly Thr
338          370          375          380
341 Leu Glu Val Val Ser Gly Cys Thr Ile Asp Met Leu Gln Ala Val Tyr
342 385          390          395          400
345 Gly Leu Asp Gly Ile Arg Leu Arg Arg Arg Gln Tyr Tyr Thr Met Pro
346          405          410          415
349 Asn Phe Arg Gln Tyr Glu Asn Arg Thr Gly His Ile Leu Val Gln Trp
350          420          425          430
353 Ser Leu Gly Ser Pro Leu His Phe Ala Gly Trp His Cys Ser Trp Cys
354          435          440          445
357 Phe Thr Pro Glu Gly Ile Tyr Phe Lys Leu Val Ser Ala Gln Asn Gly
358          450          455          460
361 Asp Phe Pro Arg Trp Gly Asp Tyr Glu Asp Lys Arg Asp Leu Asn Tyr
362 465          470          475          480
365 Ile Arg Ser Leu Ile Arg Thr Gly Gly Trp Phe Asp Gly Thr Gln Gln
366          485          490          495
369 Glu Tyr Pro Pro Ala Asp Pro Ser Glu His Met Tyr Ala Pro Lys Tyr
370          500          505          510
373 Leu Leu Lys Asn Tyr Asp Gln Phe Arg Tyr Leu Leu Glu Asn Pro Tyr
374          515          520          525
377 Arg Glu Pro Lys Ser Thr Val Glu Gly Gly Arg Arg Asn Gln Gly Ser
378          530          535          540
381 Asp Gly Arg Ser Ser Ala Val Arg Gly Lys Leu Asp Thr Thr Glu Gly
382 545          550          555          560
385 Pro Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
386          565          570
389 <210> SEQ ID NO: 14
390 <211> LENGTH: 1722
391 <212> TYPE: DNA
392 <213> ORGANISM: Artificial Sequence
394 <220> FEATURE:
395 <223> OTHER INFORMATION: Nucleotide sequence of ManII-GnTIII
397 <400> SEQUENCE: 14
398 atgtgaaga agcagtctgc agggcttgtg ctgtggggcg ctatcctctt tgtggcctgg      60
400 aatgccctgc tgctcctctt cttctggacg cgcccagcac ctggcaggcc accctcagtc      120
402 agcgctctcg atggcgaccc cgccagcctc acccggaag tgattcgctt ggcccaagac      180
404 gccgaggtgg agctggagcg gcagcgtggg ctgctgcagc agatcgggga tgccctgtcg      240
406 agccagcggg ggagggtgcc caccgcggcc cctcccggcc agccgcgtgt gcctgtgacc      300
408 cccgcgcccc tgctccagcc actgtccctt agcaaggcca ccgaagaact gcaccgggtg      360
410 gacttcgtgt tgccggagga caccacagag tattttgtgc gcaccaaagc tggcgggtgtg      420
412 tgcttcaaac caggtaccag gatgctggag aaaccttctc cagggcggac agaggagaag      480
414 accaaggtgg ctgaggggtc ctcggtccgg ggtcctgctc ggaggcctat gcggcatgtg      540

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VERIFICATION SUMMARY

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